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<110> E.I. du Pont de Nemours and Company

<120> cis-Prenyltransferases from Plants

<130> BC1019 PCT

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<150> 60/155,046

<151> 1999-09-21

<160> 37

<170> Microsoft Office 97

<210> 1

<211> 1388

<212> DNA

<213> Dimorphotheca

<400> 1

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<210> 2

<211> 287

<212> PRT

<213> Dimorphotheca

<400> 2

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Met Leu Asn Leu Pro Leu Tyr Leu Pro Lys Tyr Pro Cys Tyr Phe Pro
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Ala Ser Leu Ser Thr Asn His His Arg Gly Leu Tyr Val Phe Asn Gln
                20                      25                      30

Ser Asp Thr Thr Gly Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
 35                      40                      45

```

Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile
 50 55 60
 Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp
 65 70 75 80
 Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu
 85 90 95
 Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala
 100 105 110
 Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu
 115 120 125
 Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly
 130 135 140
 Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val
 145 150 155 160
 Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln
 165 170 175
 Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val
 180 185 190
 Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln
 195 200 205
 Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn
 210 215 220
 Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 225 230 235 240
 Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu
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 Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu
 260 265 270
 His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Arg Tyr Gly Gly
 275 280 285

<210> 3

<211> 1082

<212> DNA

<213> Calendula officinalis

<400> 3

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gaagtagaat	taccaggggg	tctcgaagaa	gaactaatgc	caaaacacgt	tgcattcata	240
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gccatgagaa	agacgcttca	atctctcctt	tttcgatgtt	ccaaattcaa	aatcaaagcg	360
gtatcgattt	atgcattttc	taccgaaaat	tggactcgcc	cgaaggaaga	agttgatttc	420
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atcgaaatag	aagaaaaatc	aagagccaat	tcaggaaccc	atgttaacta	tgactcaaac	600
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ggcgttggtg atgccacatt atatgtctta gtgtctatca gaattcgaat ttgatttata 1020
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<210> 4

<211> 228

<212> PRT

<213> Calendula officinalis

<400> 4

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Met Pro Lys His Val Ala Phe Ile Met Asp Gly Asn Arg Arg Trp Ala
 1          5          10          15

```

```

Val Glu Lys Gly Trp Ser Pro Met Thr Gly His Ser Ala Met Arg Lys
          20          25          30

```

```

Thr Leu Gln Ser Leu Leu Phe Arg Cys Ser Lys Phe Lys Ile Lys Ala
          35          40          45

```

```

Val Ser Ile Tyr Ala Phe Ser Thr Glu Asn Trp Thr Arg Pro Lys Glu
          50          55          60

```

```

Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
          65          70          75          80

```

```

Ala Glu Glu Leu Leu Ser Leu Gly Cys Arg Val Ser Ile Met Gly Lys
          85          90          95

```

```

Lys Thr Asn Leu Pro Lys Ser Leu Gln Lys Leu Cys Ile Glu Ile Glu
          100          105          110

```

```

Glu Lys Ser Arg Ala Asn Ser Gly Thr His Val Asn Tyr Ala Leu Asn
          115          120          125

```

```

Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
          130          135          140

```

```

Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
          145          150          155          160

```

```

Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
          165          170          175

```

```

Leu Val Ile Arg Thr Ser Gly Glu Ile Arg Leu Ser Asn Phe Met Leu
          180          185          190

```

```

Trp Gln Met Ala Tyr Ser Glu Leu Tyr Phe Thr Asp Lys Tyr Phe Pro
          195          200          205

```

```

Asp Phe Gly Glu Asn Asp Leu Ile Glu Ala Leu Leu Ala Phe Gln Lys
          210          215          220

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```

Val Arg Lys Cys
225

```

<210> 5

<211> 1071

<212> DNA

<213> Hevea brasiliensis

<400> 5

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gaaggagggt gtcataaggc tggattttta gctcttctga acgtactaac ttattgctat 360
gagttaggag tgaaatatgc gactatctat gccttttagca tcgataattt tcgaaggaaa 420
cctcatgagg ttcagtacgt aatggatcta atgctggaga agattgaagg gatgatcatg 480
gaagaaagta tcatcaatgc atatgatatt tgcgtacgtt ttgtgggtaa cctgaagctt 540
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aaatgtgtgc ttctcattgc tgtatgctat acttcaactg atgagatcgt gcatgctgtt 660
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<210> 6

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 6

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Met Glu Leu Tyr Asn Gly Glu Arg Pro Ser Val Phe Arg Leu Leu Gly
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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
      20              25              30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
      35              40              45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
      50              55              60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
      65              70              75              80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
      85              90              95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
      100              105              110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
      115              120              125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
      130              135              140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
      145              150              155              160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
      165              170              175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
      180              185              190

```

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285
 Leu Lys
 290

<210> 7
 <211> 1000
 <212> DNA
 <213> Hevea brasiliensis

<400> 7
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 tccctactca tattgccttc atattggatg gaaacaggag gtttgctaag aagcataaac 180
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 attccaaatg tgtgcttctc attgctgtat gctatacttc aactgatgag atcgtgcatg 540
 ctgttgaaga atcctctgaa ttgaactcca atgaagtttg taacaatcaa gaattggagg 600
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<210> 8
 <211> 290
 <212> PRT
 <213> Hevea brasiliensis

<400> 8
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 Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
 20 25 30
 Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45
 Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
 50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
 65 70 75 80
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
 100 105 110
 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140
 Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
 145 150 155 160
 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190
 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285
 Leu Lys
 290

<210> 9

<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 9

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<210> 10
 <211> 296
 <212> PRT
 <213> Hevea brasiliensis

<400> 10

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Met Glu Ile Tyr Thr Gly Gln Arg Pro Ser Val Phe Arg Ile Phe Gly
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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
          20          25          30

Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys
          35          40          45

Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala
 50          55          60

Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val
 65          70          75          80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
          85          90          95

Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
100          105          110

Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val
115          120          125

Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
130          135          140

Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
145          150          155          160

Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
          165          170          175

Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
          180          185          190

Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile
          195          200          205

Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu
210          215          220

Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr
225          230          235          240

Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn
          245          250          255

Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg
          260          265          270

His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu
275          280          285

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Glu Lys His Lys Glu Tyr Leu Lys
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<210> 11
<211> 1232
<212> DNA
<213> Vitis sp

<400> 11
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<210> 12
<211> 309
<212> PRT
<213> Vitis sp

<400> 12
Met Leu Ser Phe Arg Phe Pro Ile Ser Ala Asp Asn Ala Arg His Thr
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Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
50 55 60
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
 130 135 140

Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
 145 150 155 160

Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
 165 170 175

Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
 180 185 190

Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
 195 200 205

Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
 210 215 220

Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
 225 230 235 240

Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
 245 250 255

Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
 260 265 270

Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
 275 280 285

Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
 290 295 300

Tyr Gly Gly Arg Asn
 305

<210> 13
 <211> 1021
 <212> DNA
 <213> Oryza sativa

<400> 13

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ggctctggtc	acagggtggg	cttctctgct	ctcattgcca	gcctgctcta	ctgctatgaa	180
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aatgggtgtg	attcagacat	ttcagtggca	gatctggacc	gccatatgta	cagcgctggg	600
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ttcaagcacc	ttgtctgggc	catactccag	taccaaagag	ttcacccctc	tattgagcaa	780
agcagaaatc	tggttaagaa	gcagctgtaa	tcacatcctc	cctgggagga	gatagaaacc	840
atcatacaag	atatctgtag	ttacacaata	atctgtattc	tcctgtggta	tctcctggaa	900
tatgaaatat	ataaaggata	gctatgccat	tgtatgcttg	aacatgtgta	tgcttgagtt	960
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<210> 14
 <211> 252
 <212> PRT
 <213> Oryza sativa

<400> 14
 Met Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala
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 Lys Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser
 20 25 30
 Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr
 35 40 45
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
 50 55 60
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
 65 70 75 80
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
 85 90 95
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
 100 105 110
 Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
 115 120 125
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
 130 135 140
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
 145 150 155 160
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
 165 170 175
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
 180 185 190
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
 195 200 205
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
 210 215 220
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
 225 230 235 240
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 245 250

<210> 15
 <211> 900
 <212> DNA
 <213> Oryza sativa

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 gagttaattg cgactggtgt tcttgctagt ctgcagaatt tcatccgcaa atgcattgta 120
 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180

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agatatgcta aattcaggag tatccaggaa ggctctgggc acaggggtggg cttctctgct 240
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gaggaaaaga tcaatgaact gctagaaaac agaaatgtca tcaacaagggt taactgtaag 420
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ctgatggcta ccactgctga aaacacggga ctggctcttct ctgtttgcat gccatacaac 540
tccacttctg agattgtcaa tgcggtcaat aaggctctgtg cagaaaggag ggatatactg 600
cagagggagg atgctgacag tgttgcaaat aatgggtgtgt attcagacat ttcagtggca 660
gatctggacc gccatatgta cagcgtggt tgccccgatc ctgacattgt gatccggacc 720
tcaggtgaga ctgcctgag caatttcctt ctgtggcaga cgacgttcag tcatattgcag 780
aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840
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<210> 16

<211> 299

<212> PRT

<213> *Oryza sativa*

<400> 16

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Met Leu Gly Ser Leu Met Ser Tyr Leu Pro Ser Val Asp Ser Lys Thr
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Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
             20             25             30
Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
             35             40             45
Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
             50             55             60
Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
             65             70             75             80
Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
             85             90             95
Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
             100            105            110
Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
             115            120            125
Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
             130            135            140
Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
             145            150            155            160
Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
             165            170            175
Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
             180            185            190
Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
             195            200            205
Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
             210            215            220
His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
             225            230            235            240

```

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<400> 18
Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
  1          5          10          15
Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
          20          25          30
Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
          35          40          45
Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
          50          55          60
Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
          65          70          75          80
Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
          85          90          95

```

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
 100 105 110

Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
 115 120 125

Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
 130 135 140

Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
 145 150 155 160

Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
 165 170 175

Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
 180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
 195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
 210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
 225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
 245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
 290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg
 305 310 315 320

His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gggaactcgc	ggtgggcggc	agcgcggggc	ctgccgccga	cggacgggca	cgagcacggg	180
atgcgcgcgc	tgatgaggac	ggtgcggctc	tcccgcgcct	ggggcatccg	cgctcctcacc	240
gccttcgggt	tctcgtcga	gaactggaat	cgccccaagg	cggagggtga	cttcttgatg	300
gccttgatcg	agaggtttat	caacgacaac	ctcgcgcgag	tcttgaggga	agggaccctg	360
ctacgtataa	tcggtgaccg	ctcaaggctg	ccgatctctg	tgcagaagac	tgcacgagac	420
gccgaggagg	caacaagaaa	caactcgcag	ctcgatctag	tcctagccat	cagctacagc	480
gggcgaatgg	acattgtgca	ggcatgccgg	aatctcgccc	agaaagtggg	cgccaagctg	540
ctcaggcccg	aggacatcga	cgagtcgctg	ttcgccgacg	agctccagac	gagcgaaaca	600
tcttgcccgg	acctgctcat	caggaccagc	ggcgagctga	ggctgagcaa	cttcctgcta	660
tggcagtcgg	cttactcggg	gctcttcttc	accgacacgc	tctggcctga	tttcggggag	720
gcccaatatc	tccaagccat	gatggccttc	cagagcagag	acaggcgctt	tggaagaaga	780
aaaaacaatg	cagcgctata	aataaacggt	gcacgcgcgt	gacccgatgc	tcgatcatcc	840

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tctatctatc tgtatctgcc ttataaatca gtttttatta ccttcaaata aagtgtttct 900
ctcaagatgc gtggtgtact ataggagagg ctactaaaac ttctctccag tgattttact 960
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aaaaaa 1026
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<210> 20

<211> 266

<212> PRT

<213> Triticum aestivum

<400> 20

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Met Pro Leu Ser Asn Ser Thr Ser Ser Val Pro Ala Val Thr Val Pro
 1          5          10          15
Ala Ala Glu Glu Leu Leu Ser Gln Gly Leu Arg Ala Glu Ser Leu Pro
          20          25          30
Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
          35          40          45
Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
          50          55          60
Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
          65          70          75          80
Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
          85          90          95
Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
          100          105          110
Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
          115          120          125
Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
          130          135          140
Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
          145          150          155          160
Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
          165          170          175
Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
          180          185          190
Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
          195          200          205
Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
          210          215          220
Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
          225          230          235          240
Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
          245          250          255
Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
          260          265
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<210> 21

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Domain I of published alignment

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<222> (2)..(3)
<223> X = any amino acid

<220>
<221> UNSURE
<222> (8)
<223> X = any amino acid

<220>
<221> UNSURE
<222> (10)
<223> X = any amino acid

<300>
<301> Apfel, C. M.
<302> Use of Genomincs to Indentify Bacterial Undecaprenyl Pyrophosphate Synthetase: Clooning, Expression, and Characterization of the Essential uppS Gene
<303> J. Bacteriol.
<304> 81
<306> 483-492
<307> 1999

<400> 21
His Xaa Xaa Met Asp Gly Asn Xaa Arg Xaa Ala
1 5 10

<210> 22
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Domain V of published alignment

<220>
<221> UNSURE
<222> (3)
<223> X = any amino acid

<220>
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<222> (7)
<223> X = any amino acid

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<223> X = any amino acid

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<222> (12)
<223> X = any amino acid

<220>
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 <222> (20)..(21)
 <223> X = any amino acid

<400> 22
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Leu Trp Gln Xaa Xaa Tyr Xaa Glu
 20

<210> 23
 <211> 750
 <212> DNA
 <213> Micrococcus luteus

<300>
 <301> Shimizu, N.
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl
 Diphosphate Synthase: No Sequence Similarity between E- and
 Z-prenyl Diphosphate Synthases
 <303> J. Biol. Chem.
 <304> 273
 <306> 19476-19481
 <307> 1998

<400> 23
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 ccgcgcataa aaggacatta tgaaggcatg cagaccgtaa agaaaatcac aagatatgct 180
 agtgatttag gtgtaaagta cttaacgctg tacgcatttt caactgaaaa ttggtctcgt 240
 cctaaagatg aggttaatta cttgatgaaa ctaccgggtg atttttttaa cacattttta 300
 ccggaactca ttgaaaaaaa tgttaaagtt gaaacgattg gctttattga tgatttaccg 360
 gaccatacaa aaaaagcagt gttagaagcg aaagagaaaa cgaaacataa tacagggtta 420
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 aatgaatatt tatttacagc aaatatgcct gatcctgagt tgtaaatcag aacttccggt 600
 gaagaacggt taagtaactt ttttaatttg caatgttcat atagttagtt tgtattttata 660
 gatgaattct ggccggattt taatgaagaa agtttagcac aatgtatatc aatatatcag 720
 aatcgctcgc gacgttttgg tggattataa 750

<210> 24
 <211> 249
 <212> PRT
 <213> Micrococcus luteus

<400> 24
 Met Phe Pro Ile Lys Lys Arg Lys Ala Ile Lys Asn Asn Asn Ile Asn
 1 5 10 15
 Ala Ala Gln Ile Pro Lys His Ile Ala Ile Ile Met Asp Gly Asn Gly
 20 25 30
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
 35 40 45
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
 50 55 60
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg
 65 70 75 80

Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu
 85 90 95
 Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr
 100 105 110
 Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu
 115 120 125
 Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe
 130 135 140
 Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu
 145 150 155 160
 Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser
 165 170 175
 Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro
 180 185 190
 Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu
 195 200 205
 Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp
 210 215 220
 Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln
 225 230 235 240
 Asn Arg His Arg Arg Phe Gly Gly Leu
 245

<210> 25

<211> 861

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<308> AB013497

<400> 25

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gggaacagga gattcgctag aaagaaagag atggacgtaa aggagggcca cgaggcagga 180
tttgtagta tgagtagaat cttagaactg tggtatgaag caggagtcga tacggctacc 240
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aagggcgccg ctatagacga aagcacgtta gaatcgcatc tctacacggc gggggtaccc 600
ccttttagatt tattgattag gacaagtggc gtttccagat taagtgactt tttgatatgg 660
caggcatcga gtaagggcgt acgcatcgaa ttgctggatt gtttatggcc agagtttggg 720
cctatacggg tggcatggat tttattaaaa ttttcgtttc acaaatcctt ttttaacaaa 780
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<210> 26

<211> 286

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 26

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 Thr Lys Asn Ile Phe Ser Arg Thr Leu Arg Ala Ser Asn Cys Val Pro
 20 25 30
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
 35 40 45
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
 50 55 60
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
 65 70 75 80
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
 85 90 95
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
 100 105 110
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
 115 120 125
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
 130 135 140
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
 145 150 155 160
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
 165 170 175
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
 275 280 285

<210> 27

<211> 1032

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<308> AB013498

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<400> 27
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atgtcattaa gcttggtttc atgggtttat gtaaatcttc agaataatatt gataaaaagca 180
ttaagggtag ggccagtgcc tgaacatgtc tcctttatca tggatggtaa cggagatat 240
gccaaagtcaa gaaggctacc agtaaaaaaa ggccatgaag ctgggtgggtt aacgttacta 300
acactactgt atatctgcaa aagattgggt gtaaaatgtg tttccgccta tgcattttct 360
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aagcttgatg aattcgcaaa aagagccaag gactataagg atcccttata cggatctaaa 480
ataagaatag taggtgatca atctttacta tctccagaaa tgagaaaaaa aattaaaaaa 540
gtggaagaaa tcacacagga tggagacgat ttcactttat ttatatgttt tccttacact 600
tcaagaaatg atatgttaca tactattcgt gattcagttg aagaccattt ggaaaaataa 660
tcaccaagga ttaataataa aaaatttact aataaaatgt acatgggttt ccattccaat 720
aaatgtgaat tattaatcag aacaagtggg cataggaggc tctcagacta tatgctatgg 780
caagtacatg aaaatgccac cattgaattt agtgatacgt tgtggccaaa ttttagcttc 840
tttgctatgt acctgatgat tctcaaattg tccttctttt ccaccattca aaaatataat 900
gagaagaatc actcattgtt tgaaaaata catgaaagcg ttccttcaat atttaaaaaa 960
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ggagatgaat aa 1032

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<210> 28

<211> 343

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 28

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Met Lys Met Pro Ser Ile Ile Gln Ile Gln Phe Val Ala Leu Lys Arg
  1             5             10             15

```

```

Leu Leu Val Glu Thr Lys Glu Gln Met Cys Phe Ala Val Lys Ser Ile
      20             25             30

```

```

Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp
    35             40             45

```

```

Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly
    50             55             60

```

```

Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr
    65             70             75             80

```

```

Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly
      85             90             95

```

```

Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys
    100            105            110

```

```

Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys
    115            120            125

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```

Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu
    130            135            140

```

```

Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys
    145            150            155            160

```

```

Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys
    165            170            175

```

```

Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr
    180            185            190

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```

Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr
    195            200            205

```

Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
 210 215 220
 Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn
 225 230 235 240
 Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
 245 250 255
 Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
 260 265 270
 Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu
 275 280 285
 Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
 290 295 300
 Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys
 305 310 315 320
 Lys Lys Thr Ala Met Ser Leu Tyr Asn Phe Pro Asn Pro Pro Ile Ser
 325 330 335
 Val Ser Val Thr Gly Asp Glu
 340

<210> 29
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 29
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<210> 30
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 30
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<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 31
 gtggatccat gcttggctca cttatg 26

<210> 32
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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